

Homo sapiens
Hypothetical protein DKFZp434E0321

PubMed	Entrez	BLAST	OMIM	Taxonomy	Structure
Search <input type="text"/> Human <input type="button" value="▼"/>	<input type="button" value="display as html"/> <input type="button" value="▼"/> <input type="button" value="Go"/>			ClusterID <input type="text"/> <input type="button" value="Go"/>	

switch to text mode

NCBI Home Page

UniGene Cluster Hs.8658 FELL

UniGene

Hypothetical protein DKFZp434E0321

SEE ALSO

LocusLink: 55576

Frequently Asked Questions

HomoloGene: Hs.8658

Query Tips

SELECTED MODEL ORGANISM PROTEIN SIMILARITIES
organism, protein and percent identity and length of aligned region

Library Differential Display

H. sapiens: pir:T42681 - T42681 hypothetical protein DKFZp434E0321.1 95 % / 1099 aa

Download UniGene

M. musculus: pir:JC6506 - JC6506 tumor necrosis factor stimulated gene-6 protein - mouse 44 % / 103 aaUniGene
Homo sapiens*R. norvegicus*: pir:T13954 - T13954 MEGF6 protein - rat 32 % / 221 aa*D. melanogaster*: pir:S47008 - S47008 tenascin-like protein - fruit fly 31 % / 214 aa*C. elegans*: pir:T34513 - T34513 hypothetical protein ZK783.1 - 33 % / 228 aa
Caenorhabditis elegansNCBI Homo sapiens
UniGeneAfter some delay
Prosecution is reopened

[Home Page](#)
[Release Statistics](#)
[Library Report](#)
[Library Browser](#)

[Library Differential Display](#)

UniGene Organisms

[Homo sapiens](#)

[Mus musculus](#)

[Rattus norvegicus](#)

[Danio rerio](#)

[Bos taurus](#)

Related Resources

[Human Genome Guide](#)

[LocusLink](#)

[HomoloGene](#)

[dbEST-Database of Expressed Sequence Tags](#)

[Cancer Genome Anatomy Project](#)

[I.M.A.G.E. Quality Control](#)

MAPPING INFORMATION

Chromosome: 12

Whitehead map: WI-17715, Chr.12, 501.3 cR

UniSTS entries: A007D24 Genomic Context: [Map View](#)

UniSTS entries: H91274 Genomic Context: [Map View](#)

UniSTS entries: WI-17715 Genomic Context: [Map View](#)

EXPRESSION INFORMATION

cDNA sources: Breast, Heart, Kidney, Placenta, Spleen, head_neck

SAGE : Gene to Tag mapping

mRNA/GENE SEQUENCES (4)

AF160476	Homo sapiens CD44-like precursor FELL mRNA, complete cds	
AK024503	Homo sapiens mRNA for FLJ00112 protein, partial cds	
AL133021	Homo sapiens mRNA; cDNA DKFZp434E0321 (from clone DKFZp434E0321)	
NM_017564	Homo sapiens hypothetical protein DKFZp434E0321 (FELL), mRNA	

EST SEQUENCES (10 of 28)[Show all ESTs]

H49088	cDNA clone IMAGE:274310	3' read 3.6 kb	
AA968560	cDNA clone IMAGE:1592181	Kidney 3' read 1.7 kb	
T47504	cDNA clone IMAGE:71161	Placenta 5' read 1.4 kb	
R92610	cDNA clone IMAGE:196286	3' read 1.1 kb	
AI081595	cDNA clone IMAGE:1661049	3' read 1.0 kb	
AA010567	cDNA clone IMAGE:430269	3' read 0.9 kb	
AA004437	cDNA clone IMAGE:428667	5' read 0.8 kb	
AA004325	cDNA clone IMAGE:428667	3' read 0.8 kb	
H70480	cDNA clone IMAGE:212670	3' read 0.8 kb	
R97483	cDNA clone IMAGE:199547	5' read 0.8 kb	

Key to Symbols

Has similarity to known Proteins (after translation)

Contains a poly-Adenylation signal

Contains a mapped Sequence-tagged site (STS)

Clone source is a CGAP library

DOWNLOAD SEQUENCES

There will be a pause of up to one minute before your computer receives any data. The default filename will be "download" If your operating system responds to filename suffixes, remember to choose a suffix compatible with plain text or fasta formats.

Unix

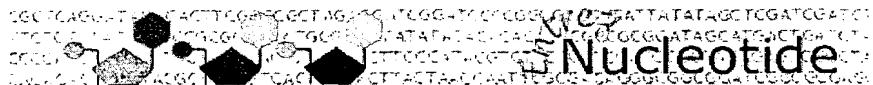


Download sequences

[Disclaimer](#) [Privacy statement](#)

Revised April 13, 2001

**Questions or Comments?
Write to the NCBI Service Desk**



PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

Search for

Limits

Index

History

Clipboard

Display

Default View

as HTML

Save

Add to Clipboard

 1: NM_017564

Homo sapiens hypothetical protein DKFZp434E0321 (FELL), mRNA

Protein, Related Sequences, Taxonomy, LinkOut

LOCUS NM_017564 3260 bp mRNA PRI 14-MAR-2001
DEFINITION Homo sapiens hypothetical protein DKFZp434E0321 (FELL), mRNA.
ACCESSION NM_017564
VERSION NM_017564.1 GI:12583704
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3260)
AUTHORS Tao, Q., Zhang, W. and Cao, X.
TITLE Molecular cloning and characterization of human FELL sharing
homology with CD44
JOURNAL Unpublished
COMMENT PREDICTED REFSEQ: The mRNA record is supported by experimental
evidence; however, the coding sequence is predicted. The reference
sequence was derived from AF160476.1.
FEATURES Location/Qualifiers
source 1..3260
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/map="12"
gene 1..3260
/gene="FELL"
/note="DKFZP434E0321"
/db_xref="LocusID:55576"
CDS 171..2864
/gene="FELL"
/codon_start=1
/db_xref="LocusID:55576"
/evidence=not_experimental
/product="CD44-like precursor FELL"
/protein_id="NP_060034.1"
/db_xref="GI:12583705"
/translation="MPQLRYHVVACHQLLENLKLISNATSLQGEPIVISVSQSTVY
INNKAKIISDIISTNGIVHIIDKLLSPKNLLITPKDNGRILQNLTTLATNNGYIKF
SNLQDSGLLSVTDPIHTPVTLFWPTDQALHALPAEQQDFLFNQDNKDKLKEYLKFH
VIRDAKVLAVDLPTSTAWTKLQGSELSVKCGAGRDIQDGLFLNGQTCTRIVQRELLFDLG
VAYGIDCLLIDPTLGGRCDFTTFDASGECGSCVNTPSCPRWSKPKGVKQKCLYNLPF
KRNLEGRERCSLVIQIPRCCKGYFGRDCQACPQGPDPAPCNNGRVCQCLDQYSATGECKC
NTGFNGTACEMCWPGRQGPDCLPQCGCSDHGQCDGQITGSGQCLCTGWTGPSCDTQAV
LPAVCTPPCSAHATCKENNTCECNLDYEGDGTCTVVDCKQDNGCAKVARCSQKGT
KVSCSCQKGYKGDGHSCTEIDPCADGLNGGCHEATCKMTGPGHKCECKSHYVGDSL
NCEPEQLPIDRLQDNQCHADAKCVDLHFQDTTVGVFHLRSPLQYKLTDFKAREAC
ANEAATMATYNQLSYAKAKYHLCASGWLETGRVAYPTAFASQNCGSGVVGIVDYGPR
PNKSEMDVFCYRMKDVNCTCKVGYVGDFGFCGSNLLQVLMSPSLTNFLTEVLAGYNS
SSARGRAFLEHLTDLISRGLTLPVQNSGLGENETLSGRDIEHHLANVSMFFYNDLVNG
TTLQTRVGSKLLTASQDPLQPTETRVDGRAILQWDIFASNGIILHVISRPLKAPPAP
VTLTHTGLGAGGIFTAILVTGAVALAAAYSFRINRRTIGFQHFSESEEDINVAALGKQQ
PENISNPILYESTTSAPPEPSYDPFTDSEERQLEGNDPLRTL"
misc_feature 177..386
/note="Fasciclin; Region: Fasciclin domain"
misc_feature 441..740
/note="Fasciclin; Region: Fasciclin domain"
misc_feature 1113..1250
/note="EGF_Lam; Region: Laminin-type epidermal growth
factor-like domain"
misc_feature 1800..2078
/note="Xlink; Region: Extracellular link domain"
misc_feature 1800..2081
/note="LINK; Region: Link (Hyaluronan-binding)"
BASE COUNT 774 a 886 c 850 g 749 t 1 others
ORIGIN

1 ggcacgagca ggagcttccc aagaacccga aaacttccca gtatcccttc cagttcagg
61 agcatttcgt gaaagatctg gtcggccag gccccttacat ctttttgcac ctttatctg
121 cagccttgtat cttggaaagct cgggttaaag actgggacaa atacgggatc atgcccagg
181 ttcttcggta ccatgtggtc gcctgcacc agctgcttgc gggaaaacctg aaattgtatc
241 caaatgtctac ttccctccaa ggagagccaa tagtcatctc cgtctctcag agcacgggt
301 atataaataa taaggctaa atcatatccaa gtatcatatc cgtactaat gggattgttc
361 atatcataga caaattgtatc tctccaaaaa atttgcttat cactccaaa gacaactctg
421 gaagaattct gaaaaatctt acgactttgg caacaaacaa tggctacatc aaatttagca
481 acttaataaca ggactcggg ttgtctggatc tcatcaccga tcccatccac accccagtc
541 ctctttctgc gcccaccgac caagccctcc atgccttacc tgctgaacaa caggacttcc
601 tggtaaaccacca agacaacaacaa gacaactgtga aggagtatttcat gtaatcgg
661 atgccaaggat ttagtctgtatc tttttccca catccactgc ctggaaagacc ctgcaagggt
721 cagactgtatc tggaaatgtt ggagctggca gggacatcgg tgacccctttt ctgaatggcc
781 aaacctgcag aattgtcag cggggatct tgggtgaccc ggggtggcc tacggcattt
841 actgtctgtatc gattgtatcc accctgggg gcccgtgtatc cacccttactt attttcgtatc
901 cctcgggggatc gtgtggggatc tggtaataatc ctcccaatc cccaaagggttgg agtaaacc
961 agggtgtatc gcaagaatgtt ctccatcaccat tggggatcttgg gggggatcttgg
1021 gggggatcttgg cggggatcttgg atacatgtcc cccatgtatc tttttttttt
1081 actgtctggatc ctggccctggatc ggacccatgttcc cccatgtatc tttttttttt
1141 atcagttactc ggccaccggatc gggggatcttggatc tttttttttt
1201 agatgtgtatc gccggggatc ttttttttttggatc tttttttttt
1261 gagatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
1321 gcccctcgatc ttttttttttggatc ttttttttttggatc tttttttttt
1381 atgcccacatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
1441 tcacatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
1501 gatgtatccatc ttttttttttggatc ttttttttttggatc tttttttttt
1561 ggcacatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
1621 acggccacatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
1681 tcggagatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
1741 atggggatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
1801 ggggtttccatc ttttttttttggatc ttttttttttggatc tttttttttt
1861 aggccatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
1921 aggccaaatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
1981 cagccatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2041 gacccaaatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2101 cctgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2161 tgatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2221 cagtcggatc ttttttttttggatc ttttttttttggatc tttttttttt
2281 ttgtgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2341 accacatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2401 aaacggggatc ttttttttttggatc ttttttttttggatc tttttttttt
2461 agaccatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2521 tcattatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2581 ctggatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2641 ctgtatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2701 aagggatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2761 tgatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2821 aagaacggatc ttttttttttggatc ttttttttttggatc tttttttttt
2881 tgccatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
2941 ttttttttttggatc ttttttttttggatc ttttttttttggatc tttttttttt
3001 tggggatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
3061 tctgtatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
3121 tacatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
3181 cccatgtatc ttttttttttggatc ttttttttttggatc tttttttttt
3241 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa

//



NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search for

Limits Index History Clipboard

Display Default View as Save Add to Clipboard

Show Items per Page

Items 1-2 of 2

One page

1: T47504 yb14f01.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:71161 5' similar to similar to SP:A41735 A41735 HYALURONATE-BINDING PROTEIN TSG-6 PRECURSOR, mRNA sequence

PubMed, Taxonomy, LinkOut

LOCUS T47504 459 bp mRNA EST 01-FEB-1995
DEFINITION yb14f01.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:71161 5' similar to similar to SP:A41735 A41735 HYALURONATE-BINDING PROTEIN TSG-6 PRECURSOR, mRNA sequence.
ACCESSION T47504
VERSION T47504.1 GI:649484
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 459)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Other_ESTs: yb14f01.s1
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1402
High quality sequence stops: 308 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1402 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 308.
FEATURES Location/Qualifiers
source 1..459
/organism="Homo sapiens"
/db_xref="GDB:492058"
/db_xref="taxon:9606"
/clone="IMAGE:71161"
/clone_lib="Stratagene placenta (#937225)"
/sex="male"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XbaI; Cloned unidirectionally. Primer: Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'"
BASE COUNT 96 a 119 c 131 g 107 t 6 others
ORIGIN
1 ctacaaccag ctccctatg cccagaaggc aagtaccacc tggctcagc aggctggctg
61 gagacccgggc ggggttgccccc ccccacagcc ttccgcctccc agaactgtgg ctctgggtgg
121 gttggatag tggactatgg acctagaccc aacaagagtg aaatgtggga tgcgttctgc
181 tatacgatgaa aagatgtgaa ctgcacctgc aagtngcta tggggagat ggcttctcat
241 gcagtggggaa acctgctgca ggtccctgtatgc tcctccctt cactcacaaa cttccctgacg
301 gaagtgtgg cctattccaa cagctcagttt cggggccgtg catttcttag gaacacntga
361 ttgacctgtt ccattccggc gcacccnttt tggggccaca gaacagtnng gttggggggga
421 gattgagacn ttttttgggg cgggacatcg gagcaacac

//



NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search **Nucleotide** for

Limits Index History Clipboard

as

1: AA257161 zr82b05.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:682161 5', mRNA sequence

Taxonomy LinkOut

LOCUS AA257161 325 bp mRNA EST 17-MAR-1997
DEFINITION zr82b05.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:682161
5', mRNA sequence.
ACCESSION AA257161
VERSION AA257161.1 GI:1891289
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 325)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
, M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlffing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
, R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham.
FEATURES Location/Qualifiers
source 1..325
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:682161"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 73 a 94 c 76 g 82 t
ORIGIN
1 ggaagagcca ttctgcagtg ggacatcttt gcctccaaatg ggatcattca tgcattttcc
61 aggcccttaa aagcacccccc tgccccccgtg accttgaccc acactggctt gggagcagg
121 atcttccttg ccatcatctt ggtgactggg gcttgctt ggctgttac tcctactttc
181 ggataaaccg gagaacaatc ggctccagc attttgatgc ggaagaggac attaatgttg
241 cagctcttgg caagcagcag cctgagaata tctcgaaccc ctgttatgag agcacaacct
301 cagctccccc agaaccttcc tacga

//